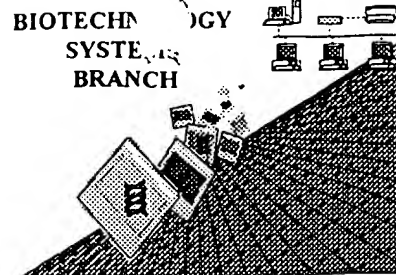


not



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/823,038

Source: OIPE

Date Processed by STIC: 4-17-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/823,038

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/823,038

DATE: 04/17/2001
TIME: 10:41:26

Input Set : A:\1037c3 SEQLIST.txt
Output Set: N:\CRF3\04172001\I823038.raw

Does Not Comply
Corrected Diskette Needed
pp. 1, 2

4 <110> APPLICANT: Strachan, Lorna
5 Sleeman, Matthew
6 Abernethy, Nevin
7 Onrust, Rene
8 Kumble, Anand
9 Murison, Greg
12 <120> TITLE OF INVENTION: Compositions isolated from stromal cells
13 and methods for their use.
16 <130> FILE REFERENCE: 11000.1037C3
C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/823,038
C--> 18 <141> CURRENT FILING DATE: 2001-03-28
18 <160> NUMBER OF SEQ ID NOS: 61
20 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

142 <210> SEQ ID NO: 6
143 <211> LENGTH: 1435
144 <212> TYPE: DNA
145 <213> ORGANISM: Mouse
147 <400> SEQUENCE: 6
148 catggggcgcc gtctggtcag ccctgctggt cggcgggggt ctagctggag cgctcatcct 60
149 gtggctgctg cggggagact ctggggcccc ggggaaagac ggggttgcg agccgcccga 120
150 gaagggcgca cctcctgggg aggctgcggc cccgggagac ggtccgggtg gtggtggcag 180
151 tggcggcctg agccctgaac cttccgatcg ggagctgggt tccaaagcag agcatcttcg 240
152 agaaagcaac ggacatttga tttctgagag caaagatctt ggtaacctgc cggaagcaca 300
153 gcggctgcag aatgttgtag cagactgggt caatgccaga gagtttggtc ctgttgggaa 360
154 gattccagac acacactcca gggccgactc tgaagcggca agaaatcaaa gccaggatc 420
155 tcatggagga gaatggagac tccccaaagg acaagaaaca gctgtcaaag tagctggcag 480
156 tgtggccgca aagctggcct ccagcagcct gcttgtagac agagctaaag cagtcagtca 540
157 ggaccaggca ggccacgagg actgggaagt ggtgtctagg cactcatctt gggggagtgt 600
158 tggtttggtt ggcagctctg aggcttctag gttaagtcta aatcagagaa tggacgacag 660
159 cacaacagct cttgtgggag gaagaggctg ggaagtagat gggaaagtgg catctctgaa 720
160 acctcaacag gtcagcatcc agttccaggt gcactacacc acaaacaccg atgtgcagtt 780
161 cattgcagtg actggagacc atgagagcct tgggagatgg aacacataca tcccactcca 840
162 ctactgcaaa gacgggctct ggtctcatte tgtcttctg cctgcagaca cagtgggtga 900
163 gtggaagtgc gtgttgtagt agaataagga agttactcgt tgggaagaat gcagcaatag 960
164 attcctgcag actggccatg aggataaagt ggttcatggg tgggtgggga ttcactgact 1020
165 cagttttcag agcatccaag aggctgcagc agaatgtgga caaggctaag gcttttagagc 1080
166 gcactgcata gcttaaagta aaggcgggtg gattccaatt gtatgcatca gggtcttttc 1140
167 agatttgcta gtgtggtctt tgtccaaaat gtatgaagat gtatgcctgc agataatgct 1200
E--> 168 tctgtgaat tggcacttgt cccttattgt attgactggt ttgtgctgac acatcaggac 1260
169 ttgagggaatt gatcatctg ggtagttgca tcttggttag tacacctgag gtatggacta 1320
170 catatgggca aggagcaact aagcaactgc acgggtacaa ggtagagcgc ccttagcagc 1380
171 tcttagacta gaaagactac aataagcccc atcaaacaca gctaaagcaa cactg 1435
2165 <210> SEQ ID NO: 61

*Missing mandatory <220> to <223>
features to explain the "n" in
the sequence. See #10 on the*

*Error
Summary
Sheet.*

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/823,038

TIME: 10:41:26

Input Set : A:\1037c3 SEQLIST.txt

Output Set: N:\CRF3\04172001\I823038.raw

2166 <211> LENGTH: 135

2167 <212> TYPE: PRT

2168 <213> ORGANISM: Mouse

2170 <400> SEQUENCE: 61

2171 Cys Gln Thr Lys Lys Lys Pro Cys Ala Pro Ala Ser Thr Leu Pro Val

2172 1 5 10 15

2173 Pro Gly His Arg Pro Pro Gly Thr Ser Arg Glu Arg Ser Gly Asp Lys

2174 20 25 30

2175 Asp Leu Pro Ser Leu Ala Val Gly Ile Cys Glu Glu His Gly Ser Ala

2176 35 40 45

2177 Met Ala Pro Gln His Ile Leu Ala Ser Gly Ser Thr Ala Gly Pro Lys

2178 50 55 60

2179 Leu Tyr Pro Lys Leu Tyr Thr Asp Val His Thr His Thr His Thr His

2180 65 70 75 80

2181 Thr Cys Thr His Thr Leu Ser Cys Gly Gly Gln Gly Ser Ser Thr Pro

2182 85 90 95

2183 Ala Cys Pro Leu Ser Val Leu Asn Thr Ala Asn Leu Gln Ala Leu Cys

2184 100 105 110

2185 Pro Glu Val Gly Ile Trp Gly Pro Arg Gln Gln Val Gly Arg Ile Glu

2186 115 120 125

2187 Asn Asn Gly Gly Arg Val Ser

2188 130 135

E-> 2193 3

→ Please delete the extraneous numeral
from the end of the file. It is causing
an invalid amino acid count for sequence
61.

VERIFICATION SUMMARY

DATE: 04/17/2001

PATENT APPLICATION: US/09/823,038

TIME: 10:41:27

Input Set : A:\1037c3 SEQLIST.txt

Output Set: N:\CRF3\04172001\I823038.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:168 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:628 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:860 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:30
L:860 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:2193 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61